

Fig. 1

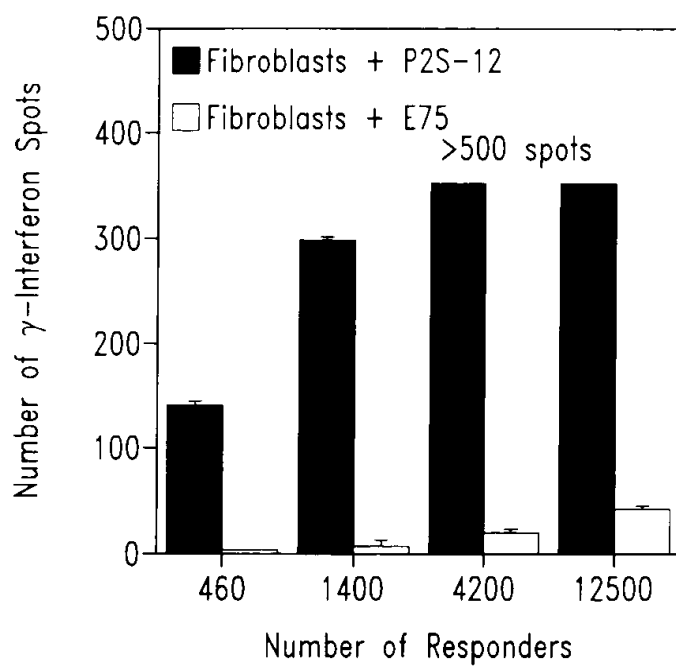


Fig. 2A

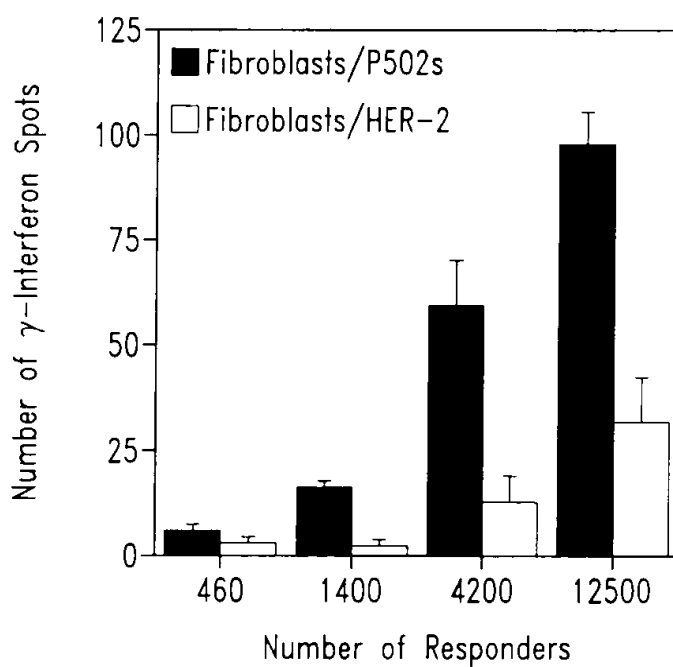


Fig. 2B

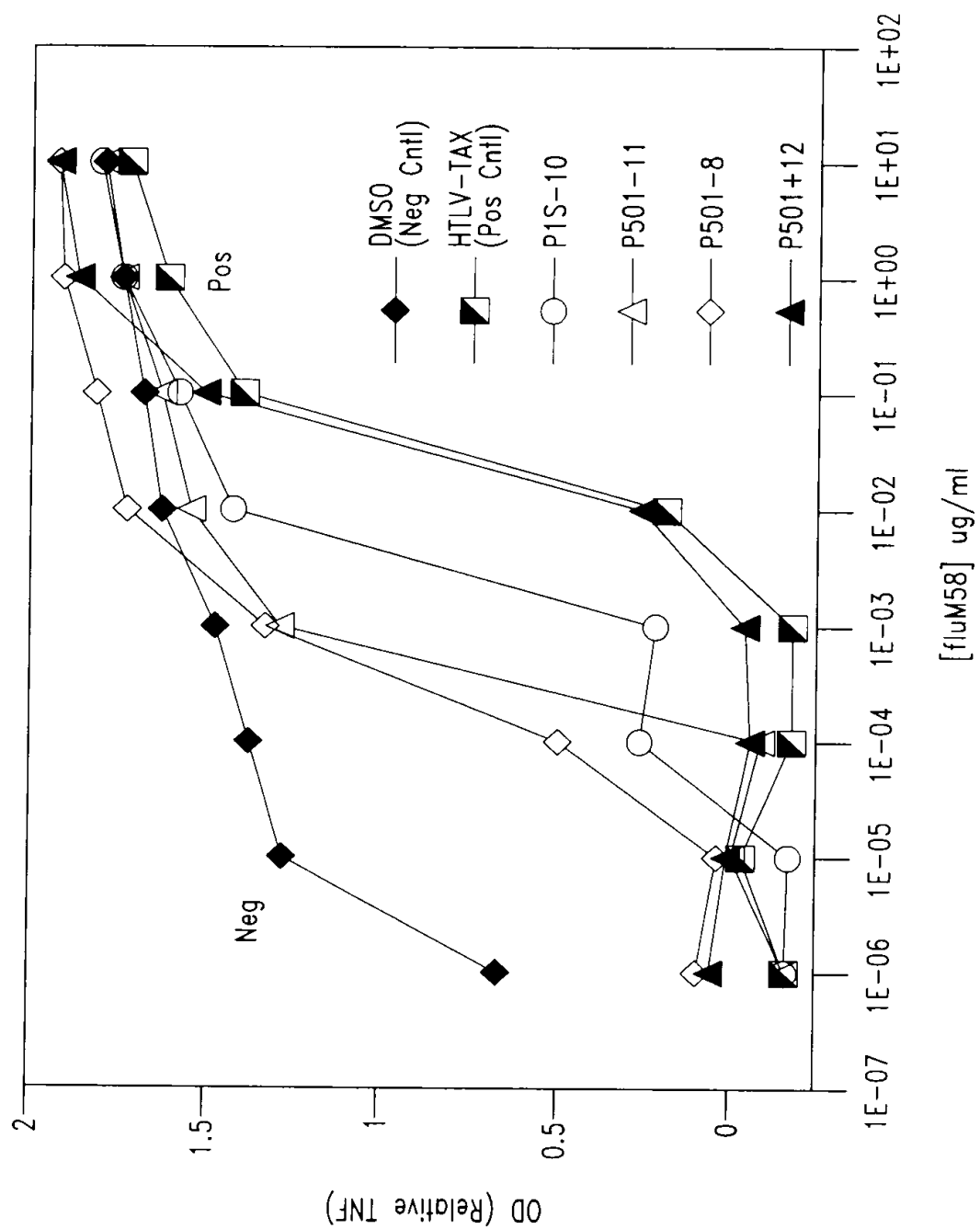


Fig. 3

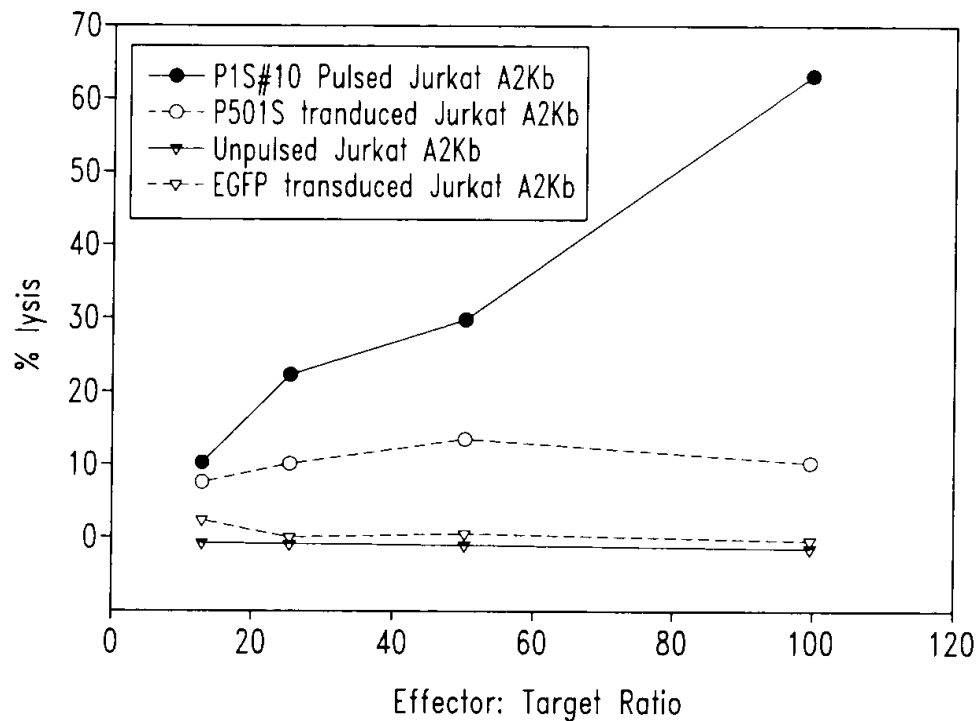


Fig. 4

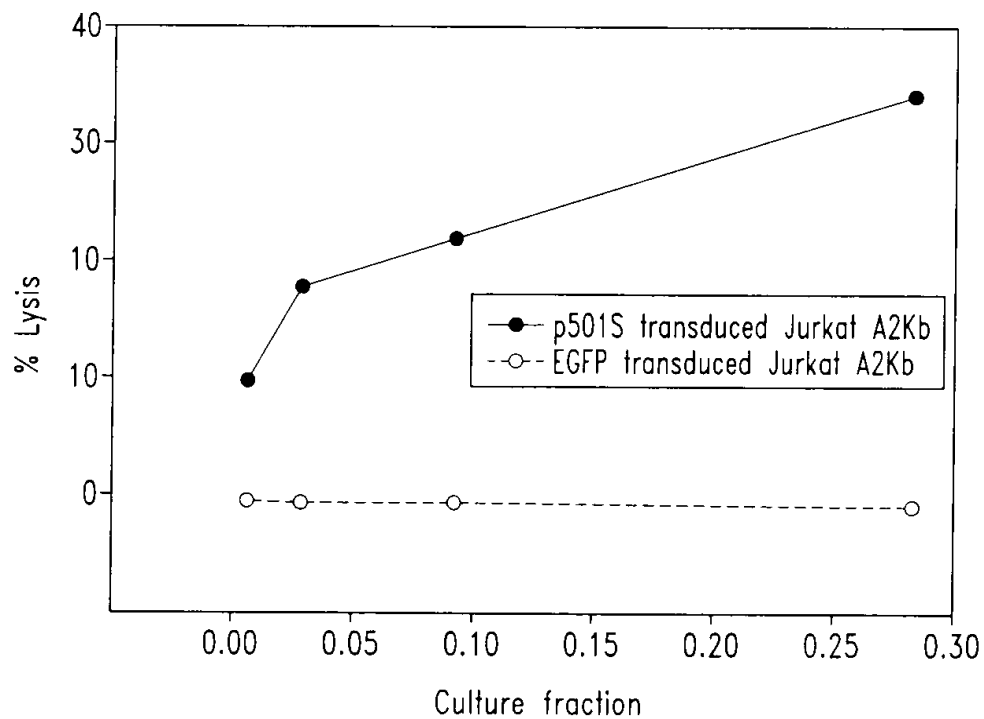


Fig. 5

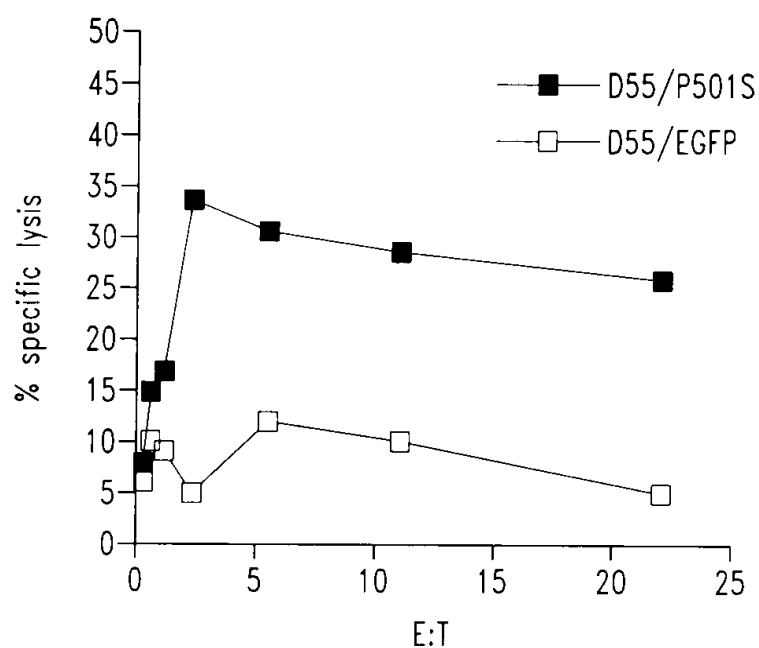


Fig. 6A

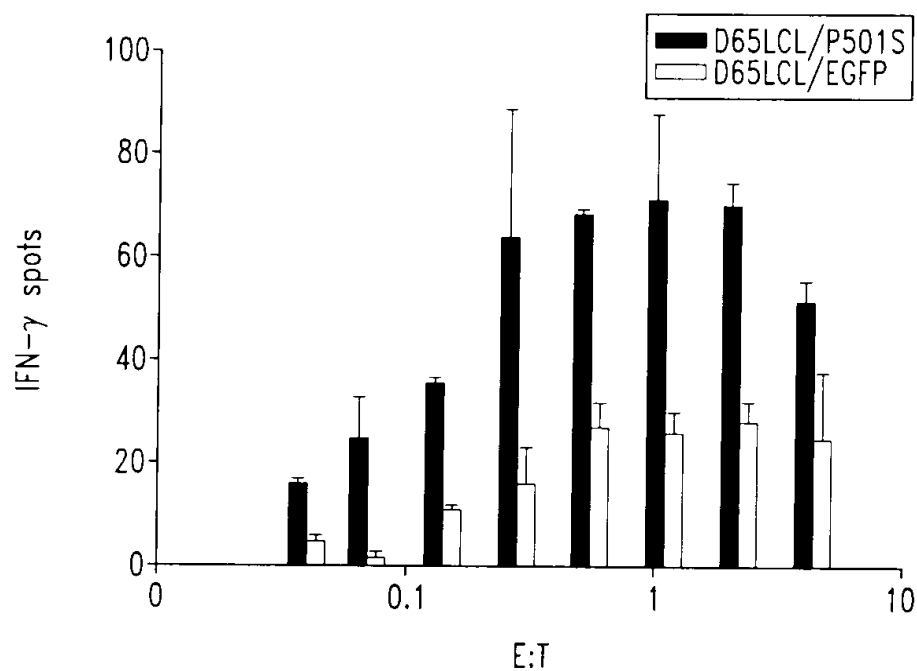
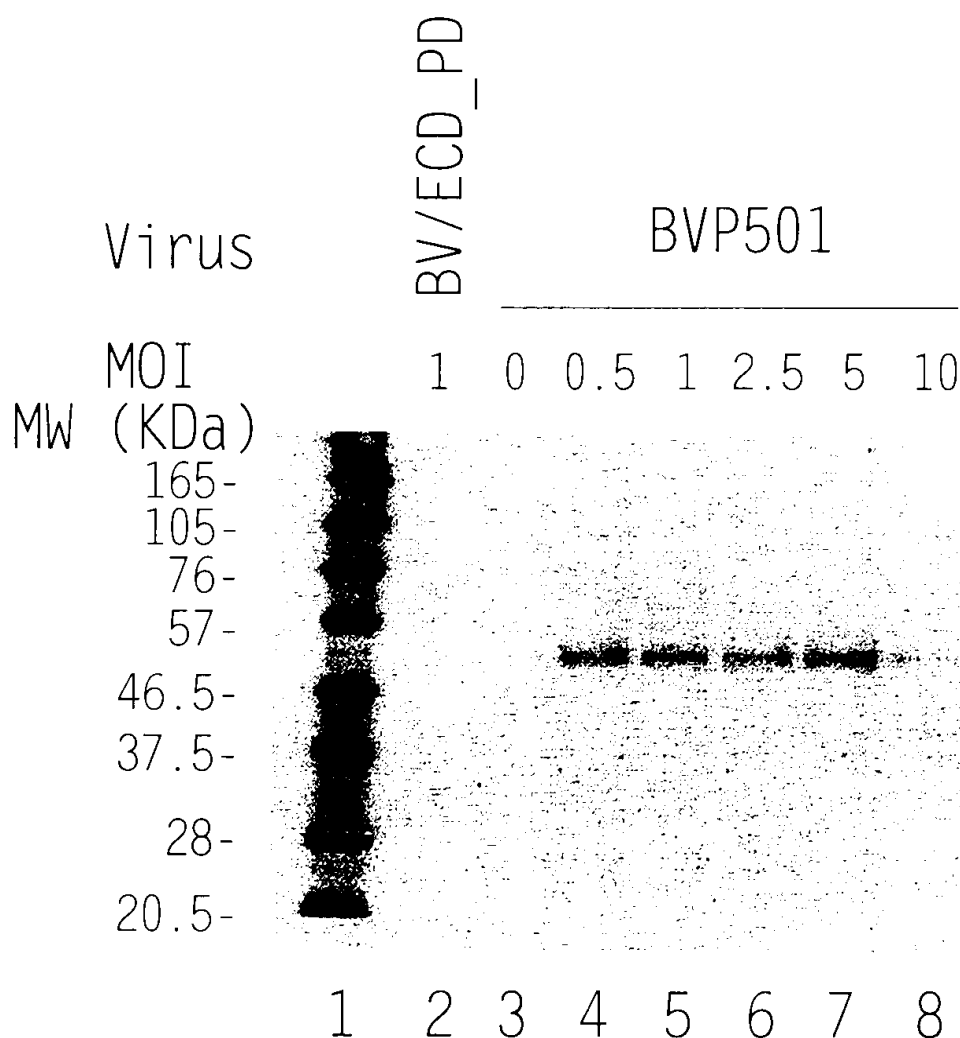


Fig. 6B

Expression of P501S
by the Baculovirus Expression System



C 6 million high 5 cells in 6-well plate were infected with an unrelated control virus BV/ECD_PD (lane2), without virus (lane3), or with recombinant baculovirus for P501 at different MOIs (lane 4-8). Cell lysates were run on SDS-PAGE under the reducing conditions and analyzed by Western blot with a monoclonal antibody against P501S (P501S-10E3-G4D3). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

Fig. 7

FIGURE 8. Mapping of the epitope recognized by 10E3-G4-D3

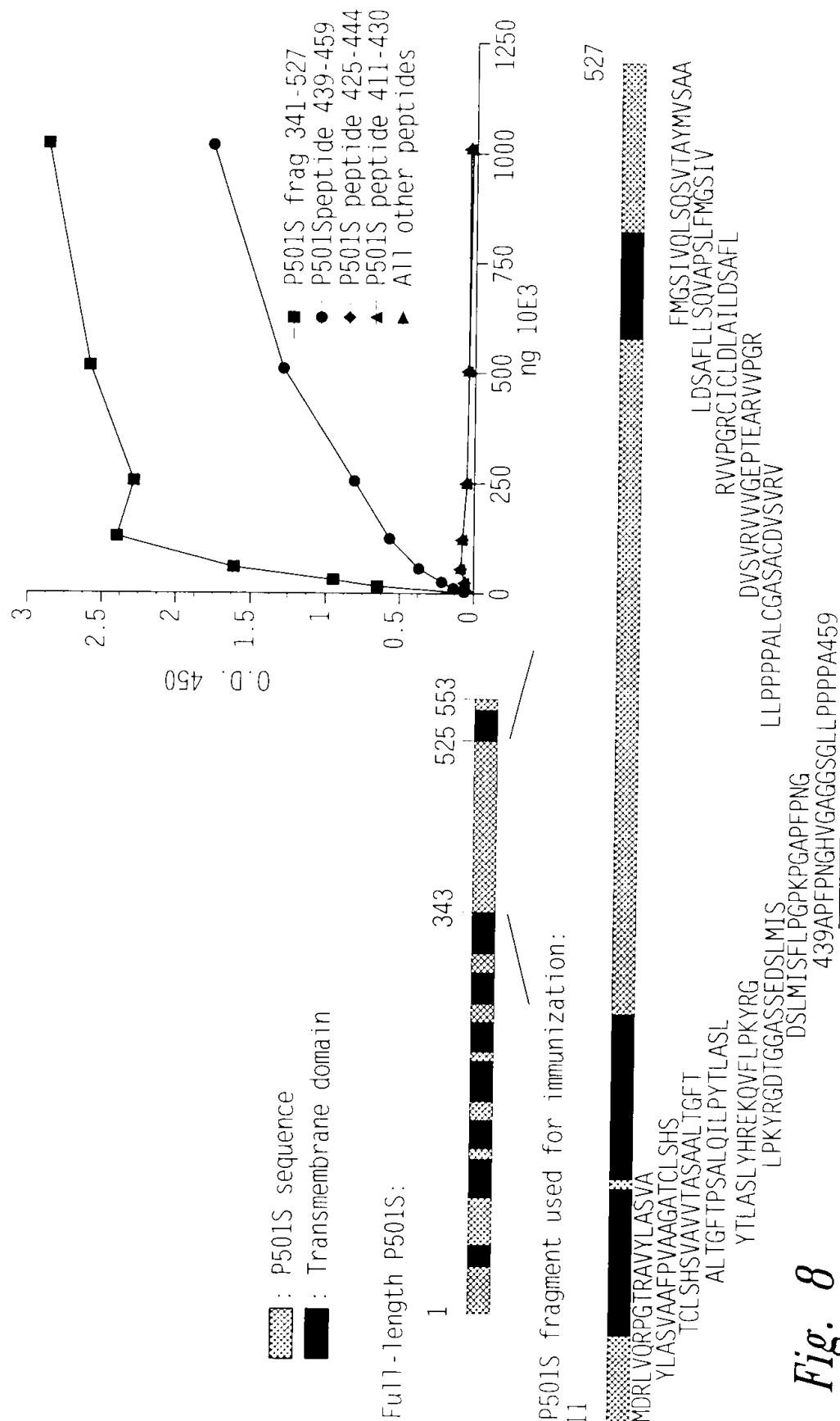


Fig. 8

Schematic of P501S with predicted
transmembrane, cytoplasmic, and extracellular regions

MVQRLWVSRLLRHRK AQLLLVNLLTFGLEVCLAAGIT **YVPPLLLLEVGVEEKFM**
TMVLGIGPVLGLVCYPLLGSAS

DHWRGRYGRRRP FIWALSLGILLSLFLIPRAGWL **AGLLCPDPRPLE** LALLILGVGLLDFCGQVCFTPL

EALLSDLFRDPDHCRQ AYSVAFMISLGGLGYLLPAI **DWDT**SALAPYLGTQEE

CLFGLLTILFLTCVAATLLV AEAAALGPTEPAEGLSAPSLSPHCCPCRARLAFRNLGALLPRL

HQLCCRMPTLRR LFVAELCSWMALMTFTLFYTDF **VGEGLYQGV**PRAEPGTEARRHYDEGVR

MGSLGLFLQCAISLVFSLVM DRLVQRFGTRAVYLAS VAAFPVAAGATCLSHSVAVVTA **SAA**

LTGFTFSALQILPYTLASLY HREKQVFLPKYRGDTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGL

LPPPPALCGASACDVSVRVVVGEPTEARVVPGRG ICLDLAILDSAFLLSQVAPSLF **MGSIVQLSQS**

VTAYMVSAAGLGLVAIYFAT QVVF**DKSD**LAKYSA

Underlined sequence: Predicted transmembrane domain; **Bold sequence**:
Predicted extracellular domain; *Italic sequence*: Predicted intracellular
domain. Sequence in bold/underlined: used generate polyclonal rabbit
serum

Localization of domains predicted using HMMTOP (G.E. Tusnady and I. Simon
(1998) Principles Governing Amino Acid Composition of Integral Membrane
Proteins: Applications to topology Prediction. J. Mol Biol. 283, 489-506.

Fig. 9

Genomic Map of (5) Corixa Candidate Genes

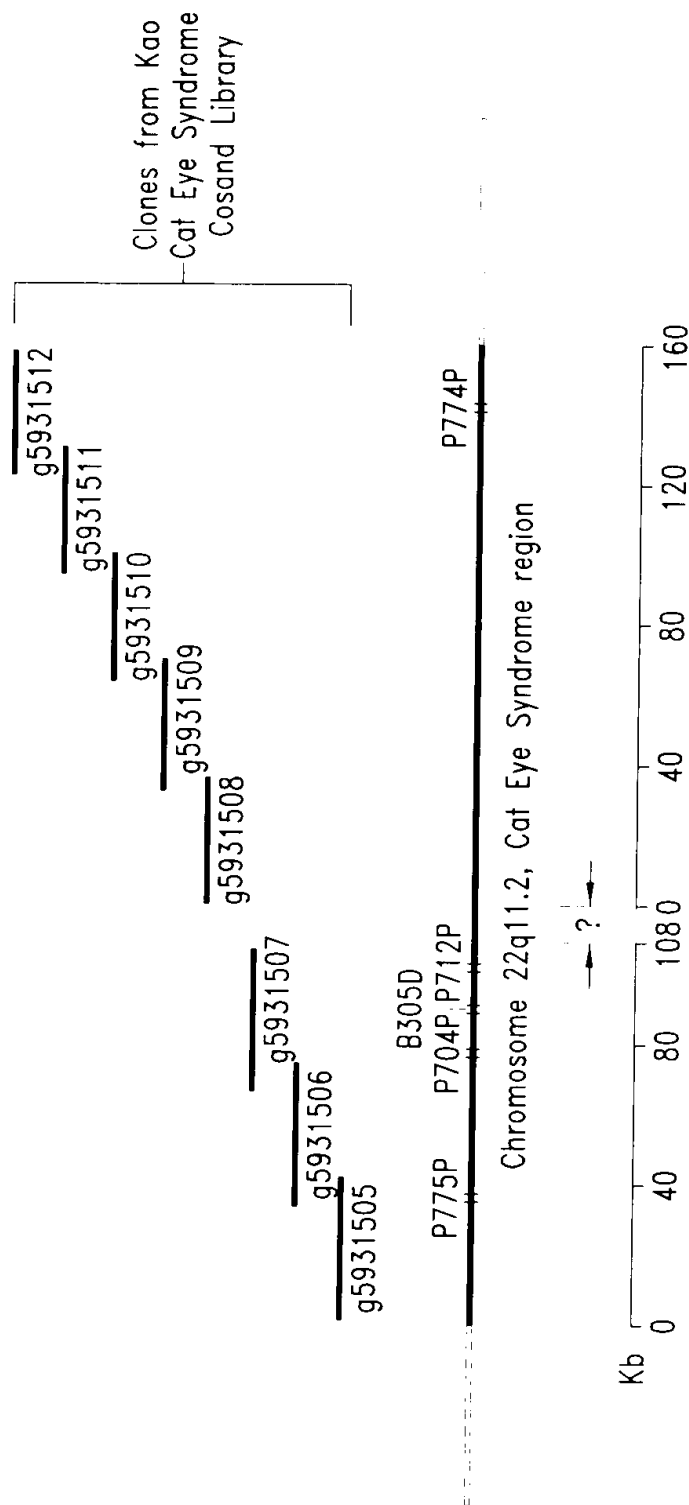


Fig. 10

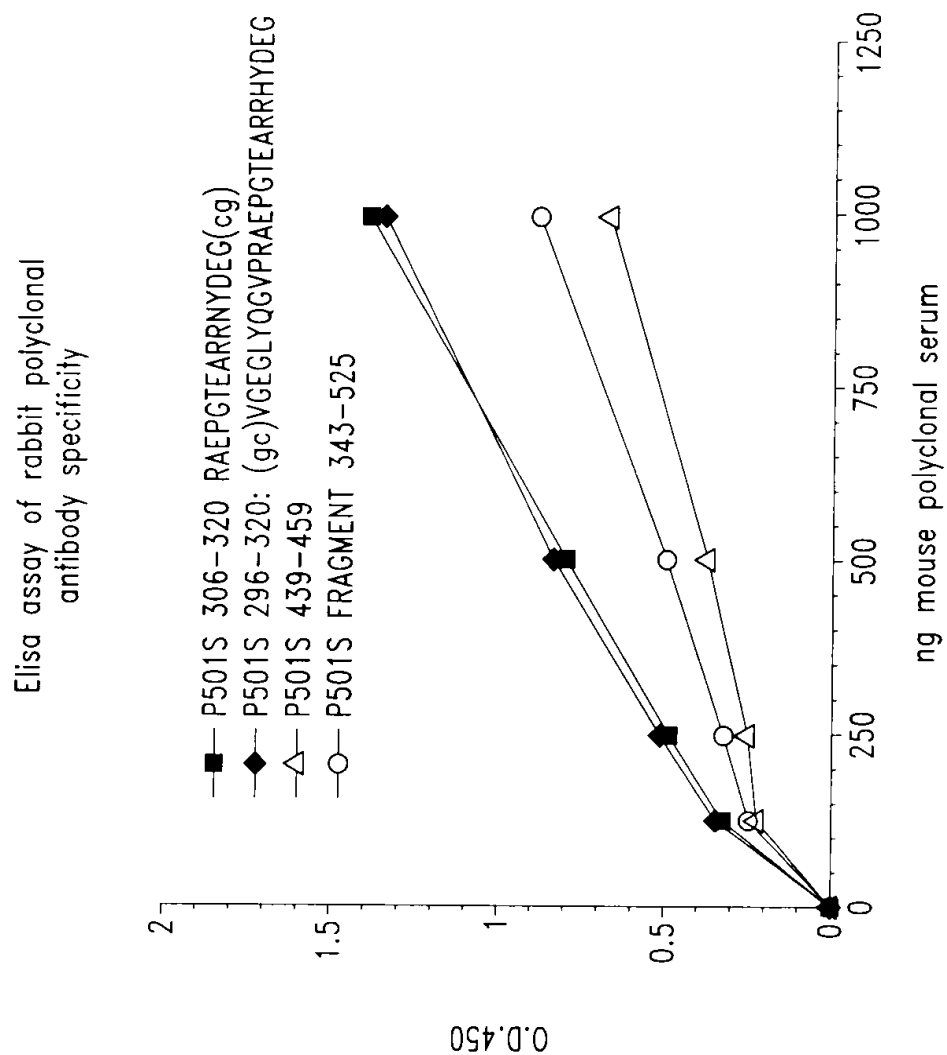


Fig. 11

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TACAGTGAAA GCGACTTGGT GAATTTTATT CAAGCAAATT TTAAGAAACG AGAATGTGTC 180
TTCTTTACCA AAGATTCCAA GGCCACGGAG AATGTGTGCA AGTGTGGCTA TGCCCAGAGC 240
CAGCACATGG AAGGCACCCA GATCAACCAA AGTGAGAAAT GGAAC TACAA GAAACACACC 300
AAGGAATTTT CTACCGACGC CTTTGGGGAT ATTGAGTTG AGACACTGGG GAAGAAAGGG 360
AAGTATATAC GTCTGTCTTG CGACACGGAC GCGGAAATCC TTTACGAGCT GCTGACCCAG 420
CACTGGCACC TGAACACACC CAACCTGGTC ATTTCTGTGA CCGGGGGCGC CAAGAACTTC 480
GCCCTGAAGC CGCGCATGCG CAAGATCTTC AGCCGGCTCA TCTACATCGC GCAGTCCAAA 540
GGTGCTTGA TTCTCACGGG AGGCACCCAT TATGGCCTGA CGAAGTACAT CGGGGAGGTG 600
GTGAGAGATA ACACCATCAG CAGGAGTTCA GAGGAGAATA TTGTGGCCAT TGGCATAGCA 660
GCTTGGGGCA TGGTCTCCAA CCGGGACACC CTCATCAGGA ATTGCGATGC TGAGGGCTAT 720
TTTTTAGCCC AGTACCTTAT GGATGACTTC ACAAGGGATC CACTGTATAT CCTGGACAAC 780
AACCACACAC ATTTGCTGCT CGTGGACAAT GGCTGTCATG GACATCCCAC TGTCGAAGCA 840
AAGCTCCGGA ATCAGCTAGA GAAGCATATC TCTGAGCGCA CTATTCAAGA TTCCAATAT 900
GGTGGCAAGA TCCCCATTGT GTGTTTTGCC CAAGGAGGTG GAAAAGAGAC TTTGAAAGCC 960
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GCTGATGTGA TCGCTAGCCT GGTGGAGGTG GAGGATGCCC CGACATCTTC TGCCGTCAAG 1080
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GCTGACCTTC AAGAAGTCAT GTTTACGGCT CTCATAAAGG ACAGACCCAA GTTTGTCCGC 1440
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GATGAAGACT TGGCAGAACA GCTGCTGGTC TATTCCTGTG AAGCTTGGGG TGGAAGCAAC 1980
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 ATTATTAAAT ATTAAAATAT CGATTTATTA TTAACCACAT TTATAAGGCT

Fig. 12A (2)

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Fig. 12B